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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=12; day=29; hr=8; min=50; sec=33; ms=591;]

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Application No: 10565058

Version No: 2.0

Input Set:**Output Set:****Started:** 2010-12-14 17:53:30.472**Finished:** 2010-12-14 17:53:34.828**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 356 ms**Total Warnings:** 41**Total Errors:** 0**No. of SeqIDs Defined:** 159**Actual SeqID Count:** 159

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Input Set:

Output Set:

Started: 2010-12-14 17:53:30.472
Finished: 2010-12-14 17:53:34.828
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 356 ms
Total Warnings: 41
Total Errors: 0
No. of SeqIDs Defined: 159
Actual SeqID Count: 159

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> University of Dundee
Hardie, David
Boudeau, Jerome
Alessi, Darlo

<120> Methods for use of an LKB1/STRAD/MO25 Complex

<130> P104299US00GP

<140> 10565058

<141> 2006-06-21

<150> PCT/GB2004/003096

<151> 2004-07-16

<150> GB 0316725.1

<151> 2003-07-17

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<170> PatentIn version 3.5

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Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile
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Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg
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Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys
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Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu
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Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg

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105

110

Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly
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Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro
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Glu Asn Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe
 145 150 155 160

Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys
 165 170 175

Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr
 180 185 190

Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly Val Ile Leu Tyr Ala
 195 200 205

Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp His Val Pro Thr Leu
 210 215 220

Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr Pro Gln Tyr Leu Asn
 225 230 235 240

Pro Ser Val Ile Ser Leu Leu Lys His Met Leu Gln Val Asp Pro Met
 245 250 255

Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln
 260 265 270

Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Ser Ser Thr
 275 280 285

Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys Glu Lys Phe Glu Cys
 290 295 300

Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn Arg Asn His Gln Asp
 305 310 315 320

Pro Leu Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met
 325 330 335

Asn Glu Ala Lys Asp Phe Tyr Leu Ala Thr Ser Pro Pro Asp Ser Phe
340 345 350

Leu Asp Asp His His Leu Thr Arg Pro His Pro Glu Arg Val Pro Phe
355 360 365

Leu Val Ala Glu Thr Pro Arg Ala Arg His Thr Leu Asp Glu Leu Asn
370 375 380

Pro Gln Lys Ser Lys His Gln Gly Val Arg Lys Ala Lys Trp His Leu
385 390 395 400

Gly Ile Arg Ser Gln Ser Arg Pro Asn Asp Ile Met Ala Glu Val Cys
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Arg Ala Ile Lys Gln Leu Asp Tyr Glu Trp Lys Val Val Asn Pro Tyr
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Tyr Leu Arg Val Arg Arg Lys Asn Pro Val Thr Ser Thr Tyr Ser Lys
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Met Ser Leu Gln Leu Tyr Gln Val Asp Ser Arg Thr Tyr Leu Leu Asp
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Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu Ala Lys Ser Gly Thr Ala
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Thr Pro Gln Arg Ser Gly Ser Val Ser Asn Tyr Arg Ser Cys Gln Arg
485 490 495

Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys Ser Ser Glu Val Ser Leu
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Thr Ser Ser Val Thr Ser Leu Asp Ser Ser Pro Val Asp Leu Thr Pro
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<213> Homo sapiens

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His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val
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Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile
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Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg
50 55 60

Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys
65 70 75 80

Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu
85 90 95

Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg
100 105 110

Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly
115 120 125

Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro
130 135 140

Glu Asn Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe
145 150 155 160

Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys
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Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr
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Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly Val Ile Leu Tyr Ala

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Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp His Val Pro Thr Leu
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Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr Pro Gln Tyr Leu Asn
 225 230 235 240

Pro Ser Val Ile Ser Leu Leu Lys His Met Leu Gln Val Asp Pro Met
 245 250 255

Lys Arg Ala Ser Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln
 260 265 270

Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Ser Ser Thr
 275 280 285

Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys Glu Lys Phe Glu Cys
 290 295 300

Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn Arg Asn His Gln Asp
 305 310 315 320

Pro Leu Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met
 325 330 335

Asn Glu Ala Lys Asp Phe Tyr Leu Ala Thr Ser Pro Pro Asp Ser Phe
 340 345 350

Leu Asp Asp His His Leu Thr Arg Pro His Pro Glu Arg Val Pro Phe
 355 360 365

Leu Val Ala Glu Thr Pro Arg Ala Arg His Thr Leu Asp Glu Leu Asn
 370 375 380

Pro Gln Lys Ser Lys His Gln Gly Val Arg Lys Ala Lys Trp His Leu
 385 390 395 400

Gly Ile Arg Ser Gln Ser Arg Pro Asn Asp Ile Met Ala Glu Val Cys
 405 410 415

Arg Ala Ile Lys Gln Leu Asp Tyr Glu Trp Lys Val Val Asn Pro Tyr
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Tyr Leu Arg Val Arg Arg Lys Asn Pro Val Thr Ser Thr Tyr Ser Lys
435 440 445

Met Ser Leu Gln Leu Tyr Gln Val Asp Ser Arg Thr Tyr Leu Leu Asp
450 455 460

Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu Ala Lys Ser Gly Thr Ala
465 470 475 480

Thr Pro Gln Arg Ser Gly Ser Val Ser Asn Tyr Arg Ser Cys Gln Arg
485 490 495

Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys Ser Ser Glu Val Ser Leu
500 505 510

Thr Ser Ser Val Thr Ser Leu Asp Ser Ser Pro Val Asp Leu Thr Pro
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Arg Pro Gly Ser His Thr Ile Glu Phe Phe Glu Met Cys Ala Asn Leu
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Ile Lys Ile Leu Ala Gln
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<212> PRT
<213> Homo sapiens

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His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val
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Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile
35 40 45

Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg
50 55 60

Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys
65 70 75 80

Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu
85 90 95

Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg
100 105 110

Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly
115 120 125

Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro
130 135 140

Glu Asn Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe
145 150 155 160

Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys
165 170 175

Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr
180 185 190

Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly Val Ile Leu Tyr Ala
195 200 205

Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp His Val Pro Thr Leu
210 215 220

Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr Pro Gln Tyr Leu Asn
225 230 235 240

Pro Ser Val Ile Ser Leu Leu Lys His Met Leu Gln Val Asp Pro Met
245 250 255

Lys Arg Ala Ser Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln
260 265 270

Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Ser Ser Thr
275 280 285

Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys Glu Lys Phe Glu Cys

290

295

300

Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn Arg Asn His Gln Asp
305 310 315 320

Pro Leu Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met
325 330 335

Asn Glu Ala Lys Asp Phe Tyr Leu Ala Thr Ser Pro Pro Asp Ser Phe
340 345 350

Leu Asp Asp His His Leu Thr Arg Pro His Pro Glu Arg Val Pro Phe
355 360 365

Leu Val Ala Glu Thr Pro Arg Ala Arg His Thr Leu Asp Glu Leu Asn
370 375 380

Pro Gln Lys Ser Lys His Gln Gly Val Arg Lys Ala Lys Trp His Leu
385 390 395 400

Gly Ile Arg Ser Gln Ser Arg Pro Asn Asp Ile Met Ala Glu Val Cys
405 410 415

Arg Ala Ile Lys Gln Leu Asp Tyr Glu Trp Lys Val Val Asn Pro Tyr
420 425 430

Tyr Leu Arg Val Arg Arg Lys Asn Pro Val Thr Ser Thr Tyr Ser Lys
435 440 445

Met Ser Leu Gln Leu Tyr Gln Val Asp Ser Arg Thr Tyr Leu Leu Asp
450 455 460

Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu Ala Lys Ser Gly Thr Ala
465 470 475 480

Thr Pro Gln Arg Ser Gly Ser Val Ser Asn Tyr Arg Ser Cys Gln Arg
485 490 495

Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys Ser Ser Glu Val Ser Leu
500 505 510

Thr Ser Ser Val Thr Ser Leu Asp Ser Ser Pro Val Asp Leu Thr Pro
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Arg Pro Gly Ser His Thr Ile Glu Phe Phe Glu Met Cys Ala Asn Leu
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Ile Lys Ile Leu Ala Gln
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Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr
35 40 45

Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val
50 55 60

Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu
65 70 75 80

Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp
85 90 95

Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn
100 105 110

Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu
115 120 125

Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser
130 135 140

Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly
145 150 155 160

Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu
165 170 175

Cys Gly Thr Leu Pro Phe Asp Asp Glu His Val Pro Thr Leu Phe Lys
180 185 190

Lys Ile Arg Gly Gly Val Phe Tyr Ile Pro Glu Tyr Leu Asn Arg Ser
195 200 205

Val Ala Thr Leu Leu Met His Met Leu Gln Val Asp Pro Leu Lys Arg
210 215 220

Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln Asp Leu
225 230 235 240

Pro Ser Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Asp Ala Asn Val Ile
245 250 255

Asp Asp Glu Ala Val Lys Glu Val Cys Glu Lys Phe Glu Cys Thr Glu
260 265 270

Ser Glu Val Met Asn Ser Leu Tyr Ser Gly Asp Pro Gln Asp Gln Leu
275 280 285

Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met Asn Gln
290 295 300

Ala Ser Glu Phe Tyr Leu Ala Ser Ser Pro Pro Ser Gly Ser Phe Met
305 310 315 320

Asp Asp Ser Ala Met His Ile Pro Pro Gly Leu Lys Pro His Pro Glu
325 330 335

Arg Met Pro Pro Leu Ile Ala Asp Ser Pro Lys Ala Arg Cys Pro Leu
340 345 350

Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val Lys Lys Ala
355 360